AMENDMENTS

In the claims:

Please cancel claims 30-60 without prejudice or disclaimer, and please amend claim 25, as set forth in the following complete listing of the claims, which replaces all other listings of the claims.

1 (Original). A method for identifying a subject at risk of osteoarthritis, which comprises detecting the presence or absence of one or more polymorphic variations associated with osteoarthritis in a nucleic acid sample from a subject, wherein the one or more polymorphic variations are detected in a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A, or a substantially identical sequence thereof, or a fragment of the foregoing;

whereby the presence of the polymorphic variation is indicative of the subject being at risk of osteoarthritis.

2 (Original). The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 31118000 to 31129000 of chromosome 16 in human genomic DNA.

4 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 1 selected from the group consisting of 247, 1535, 2386, 6440, 9133, 9143, 9471, 13150, 13717, 14466, 15769, 16870, 18545, 18749, 19123, 20736, 21038, 21046, 21050, 21056, 21706, 23170, 25028, 27871, 28070, 31717, 32019, 32318, 33080, 33101, 34236, 34285, 34818, 35168, 37981, 38113, 38117, 38481, 38615, 38944, 39288, 41385, 42136, 42185, 42353, 42434, 44580, 44675, 45739, 46439, 47457, 47735, 50319, 50708, 51185, 53002, 53064, 53637, 55274, 55825, 55986, 56684, 57653, 57659, 57692, 57775, 61313, 61431, 61699, 62906, 63619, 64664, 68452, 69665, 69681, 70091, 74637, 74760, 76523, 78559, 79549, 79882, 81339, 81681, 81696, 83517, 85431, 86332, 87358, 87725, 89052, 90020, 90231, 90284, 90447, 90601, 90724, 92559, 95176, 95195 and 96822.

5 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 1 selected from the group consisting of 13150, 21046, 23170, 25028, 44580, 62906, 64664 and 83517.

6 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 36914000 to 36931000 of chromosome 4 in human genomic DNA.

7 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 2 selected from the group consisting of 211, 7217, 7895, 13308, 14279, 17026, 18271, 20417, 21843, 22069, 22145, 22519, 22539, 23236, 23256, 23402, 23499, 23620, 23871, 24136, 25427, 25866, 26541, 26576, 26689, 26720, 27113, 27164, 27186, 28341, 29160, 29844, 30665, 30830, 31061, 31523, 32326, 32346, 32358, 34909, 34975, 35066, 35096, 35375, 36304, 36712, 36770, 37342, 37412, 37884, 38077, 38300, 38301, 41189, 44408, 44493, 44571, 44670, 45219, 45258, 47261, 48473, 48771, 55292, 56479, 56747, 60620, 60688, 61058, 61129, 61577, 61961, 63351, 63926, 65798, 66043, 66044, 66246, 66318, 66547, 71238, 71283, 71492, 72274, 73762, 74209, 75284, 77347, 77589, 78096, 78606, 78862, 79135, 79146, 79456, 79609, 80086, 80119, 80766, 81110, 81269, 81668, 82433, 82559, 83298, 83821, 84121, 84147, 84543, 84554, 84691, 84727, 85678, 86699, 86700, 86792, 86832, 87045, 87140, 87365, 88342, 88498, 88589, 95502, 96968, 97448, 97568 and 98724.

8 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 2 selected from the group consisting of 23236, 32358, 47261, 48771, 55292, 60688, 72274, 74209, 77589, 79135, 79456, 79609, 80119, 80766, 81110, 82433, 84121, 84147, 85678, 86699, 86832, 87140 and 88589.

9 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 170719500 to 170766500 of chromosome 6 in human genomic DNA.

10 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 3 selected from the group consisting of 229, 6310, 11840, 11870, 12064, 13392, 16354, 16559, 16935, 17616, 17737, 18321, 18453, 18811,

20020, 21662, 23197, 23446, 24339, 25504, 27174, 28008, 29294, 29759, 30832, 44512, 44850, 45884, 46345, 48589, 53371, 53911, 53990, 55152, 55667, 58952, 59315, 60029, 61477, 62988, 63090, 64021, 65685, 70220, 70323, 70959, 73436, 82945, 82958, 82961, 82964, 82965, 83006, 83025, 83034, 83074 ,83132, 83155, 83172, 83174, 83206, 83216, 83234, 83252, 83260, 83263, 83296, 83319, 83322, 83324, 83357, 83375, 83381, 83389, 83443, 83499, 83545, 83566, 83591, 83619, 83698, 83780, 83784, 83826, 83832, 83852, 86297, 86315, 86420, 86460, 86714, 86718, 86736, 86753, 86766, 88162, 88218, 88246, 88255, 88309, 88310, 88471, 88619, 88904, 89044, 90531, 90534, 90613 and 46252.

11 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 3 selected from the group consisting of 229, 6310, 16559, 18453, 25504, 27174, 30832, 44850, 45884, 48589, 61477, 82961 and 46252.

12 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 27963000 to 27983000 of chromosome 8 in human genomic DNA.

13 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 4 selected from the group consisting of 211, 473, 1536, 5639, 17186, 17335, 25029, 25111, 28811, 28863, 30809, 40985, 45147, 45282, 46168, 46328, 49077, 51925, 52141, 52168, 60852, 62468, 65572, 79089, 79541, 79790, 90843, 90978, 91052, 91131, 91132, 94439 and 94621.

14 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 4 selected from the group consisting of 40985, 46168, 51925 and 52168.

15 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 44962000 to 45013000 of chromosome 13 in human genomic DNA.

16 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 5 selected from the group consisting of 243,

10208, 15049, 15111, 15272, 15287, 15326, 15327, 17038, 19391, 21702, 22431, 22881, 27744, 32564, 32698, 33104, 33181, 33256, 33543, 35567, 40085, 40482, 45641, 46059, 48504, 48919, 49693, 49874, 50020, 50616, 50719, 55511, 65533, 70529, 75591, 77266, 80368, 82475, 92462, 92480, 95819 and 96275.

17 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 5 selected from the group consisting of 15111, 45641, 46059, 49693, 49874, 50020, 50719, 70529, 82475, 92462, 92480 and 96275.

18 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 76196500 to 76221500 of chromosome 14 in human genomic DNA.

19 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 6 selected from the group consisting of 218, 1440, 1442, 2611, 4317, 4724, 4788, 5202, 5780, 5974, 6644, 7430, 7938, 8095, 8183, 8312, 8352, 9348, 9378, 9617, 9727, 9834, 9899, 10211, 10377, 10695, 10729, 10730, 11433, 11951, 12697, 12982, 14419, 14501, 14983, 15280, 15475, 15888, 15976, 16307, 16442, 17255, 18948, 19435, 19753, 20021, 20022, 20503, 20590, 21804, 21919, 21990, 22412, 22536, 23432, 23468, 23772, 24325, 24773, 26274, 27440, 28561, 30071, 31764, 33008, 35310, 35460, 37112, 37285, 37747, 38057, 38859, 38860, 39525, 40216, 40281, 41453, 42091, 42513, 42935, 42985, 43003, 43281, 43716, 43866, 44234, 44596, 44871, 45005, 45282, 47178, 47816, 47887, 48134, 48135, 48276, 48400, 48798, 48803, 49146, 49969, 51059, 51064, 53285, 54560, 54748, 54785, 55102, 55644, 55705, 55841, 56623, 56825, 56827, 56892, 59150, 59958, 60231, 60524, 61871, 62226, 63230, 63468, 63787, 65732, 65989, 68832, 69904, 70365, 70886, 73088, 73103, 75934, 75966, 76273, 77943, 78466, 78861, 78872, 79836, 80908, 81509, 83576, 83662, 83782, 84282, 84444, 85129, 85151, 85296, 85809, 86387, 86494, 89786, 89894, 90122, 92067, 92187, 92312, 92824, 93733, 96553 and 96941.

20 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 6 selected from the group consisting of 4788, 8312, 9378, 9727, 9899, 10211, 27440, 40216, 40281, 42091, 43866, 48803, 51059, 55644, 56623, 73103, 78872, 79836, 85129, 92824 and 96941.

21 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 38830000 to 38844000 of chromosome 21 in human genomic DNA.

22 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 7 selected from the group consisting of 231, 882, 960, 1194, 1530, 1673, 2096, 2285, 5873, 7256, 7988, 8222, 8381, 8814, 8915, 9642, 9902, 10619, 10927, 11032, 14377, 15608, 15928, 16296, 17598, 19272, 20084, 20577, 28051, 29466, 29530, 29987, 30012, 30322, 32216, 32516, 32544, 32746, 33137, 33538, 33798, 33802, 33964, 34132, 34210, 34317, 34499, 34753, 34845, 35335, 36423, 36450, 36481, 38447, 38784, 39387, 39458, 39822, 40305, 40869, 40926, 41010, 41134, 41984, 42172, 42753, 43011, 43176, 43320, 43381, 44142, 44383, 44726, 45087, 45141, 45359, 45421, 45456, 45467, 45486, 45709, 45716, 47626, 49413, 49796, 49962, 50075, 50093, 50571, 50615, 50780, 50851, 51459, 53193, 53702, 53736, 53795, 54109, 54126, 54230, 54894, 55455, 55499, 56522, 56662, 56954, 57267, 58282, 58916, 59544, 59666, 59913, 66846, 67245, 67652, 67955, 67966, 68420, 70226, 70810, 72246, 73330, 73457, 74389, 74638, 74640, 75358, 75952, 76098, 77836, 78449, 78507, 80031, 81695, 82775, 82795, 84611, 84657, 84693, 85020, 85048, 85100, 85325, 85452, 85868, 85936, 85990, 86139, 86497, 87236, 87248, 87533, 87912, 88108, 88494, 89598, 90235, 91287, 91359, 92384, 92410, 92900, 94495, 94512, 97777 and 98333.

23 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 7 selected from the group consisting of 1673, 20577, 33137, 39822, 45716, 49962, 51459, 54894, 55455, 55499, 58282, 68420 and 80031.

24 (Original). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in Table A.

25 (Currently Amended). The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in linkage disequilibrium with one or more positions in claim 4~~, 7, 10, 13, 16, 19, 22 or 24~~.

26 (Original). The method of claim 1, wherein detecting the presence or absence of the one or more polymorphic variations comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of a polymorphic variation in the extension products.

27 (Original). The method of claim 1, wherein the subject is a human.

28 (Original). The method of claim 27, wherein the subject is a human female.

29 (Original). The method of claim 27, wherein the subject is a human male.

30-60 (Cancelled).